

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/562,776
Source: 1FwP
Date Processed by STIC: 1/10/06

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/562,776

DATE: 01/10/2006
TIME: 08:50:37

Input Set : A:\248832.ST25.txt
Output Set: N:\CRF4\01102006\J562776.raw

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3 <110> APPLICANT: Kuroita, Toshihiro
4           Sogabe, Atsushi
5           Takarada, Yutaka
6           Tanaka, Naoki
8 <120> TITLE OF INVENTION: PROTEIN ACHIEVING IMPROVED BLOCKING EFFICIENCY
10 <130> FILE REFERENCE: 248832
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/562,776
C--> 12 <141> CURRENT FILING DATE: 2005-12-29
12 <150> PRIOR APPLICATION NUMBER: PCT/JP04/09785
13 <151> PRIOR FILING DATE: 2004-07-02
15 <150> PRIOR APPLICATION NUMBER: JP 2003-191081
16 <151> PRIOR FILING DATE: 2003-07-03
18 <160> NUMBER OF SEQ ID NOS: 17
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 638
24 <212> TYPE: PRT
25 <213> ORGANISM: Escherichia coli
27 <400> SEQUENCE: 1
29 Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val
30 1           5           10          15
33 Ala Ile Met Asp Gly Thr Thr Pro Arg Val Leu Glu Asn Ala Glu Gly
34 20          25          30
37 Asp Arg Thr Thr Pro Ser Ile Ile Ala Tyr Thr Gln Asp Gly Glu Thr
38 35          40          45
41 Leu Val Gly Gln Pro Ala Lys Arg Gln Ala Val Thr Asn Pro Gln Asn
42 50          55          60
45 Thr Leu Phe Ala Ile Lys Arg Leu Ile Gly Arg Arg Phe Gln Asp Glu
46 65          70          75          80
49 Glu Val Gln Arg Asp Val Ser Ile Met Pro Phe Lys Ile Ile Ala Ala
50 85          90          95
53 Asp Asn Gly Asp Ala Trp Val Glu Val Lys Gly Gln Lys Met Ala Pro
54 100         105         110
57 Pro Gln Ile Ser Ala Glu Val Leu Lys Met Lys Lys Thr Ala Glu
58 115         120         125
61 Asp Tyr Leu Gly Glu Pro Val Thr Glu Ala Val Ile Thr Val Pro Ala
62 130         135         140
65 Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Arg Ile
66 145         150         155          160
69 Ala Gly Leu Glu Val Lys Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala
70 165         170         175
73 Leu Ala Tyr Gly Leu Asp Lys Gly Thr Gly Asn Arg Thr Ile Ala Val
74 180         185         190

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77 Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Ile Glu Ile Asp
78 195 200 205
81 Glu Val Asp Gly Glu Lys Thr Phe Glu Val Leu Ala Thr Asn Gly Asp
82 210 215 220
85 Thr His Leu Gly Gly Glu Asp Phe Asp Ser Arg Leu Ile Asn Tyr Leu
86 225 230 235 240
89 Val Glu Glu Phe Lys Lys Asp Gln Gly Ile Asp Leu Arg Asn Asp Pro
90 245 250 255
93 Leu Ala Met Gln Arg Leu Lys Glu Ala Ala Glu Lys Ala Lys Ile Glu
94 260 265 270
97 Leu Ser Ser Ala Gln Gln Thr Asp Val Asn Leu Pro Tyr Ile Thr Ala
98 275 280 285
101 Asp Ala Thr Gly Pro Lys His Met Asn Ile Lys Val Thr Arg Ala Lys
102 290 295 300
105 Leu Glu Ser Leu Val Glu Asp Leu Val Asn Arg Ser Ile Glu Pro Leu
106 305 310 315 320
109 Lys Val Ala Leu Gln Asp Ala Gly Leu Ser Val Ser Asp Ile Asp Asp
110 325 330 335
113 Val Ile Leu Val Gly Gly Gln Thr Arg Met Pro Met Val Gln Lys Lys
114 340 345 350
117 Val Ala Glu Phe Phe Gly Lys Glu Pro Arg Lys Asp Val Asn Pro Asp
118 355 360 365
121 Glu Ala Val Ala Ile Gly Ala Ala Val Gln Gly Gly Val Leu Thr Gly
122 370 375 380
125 Asp Val Lys Asp Val Leu Leu Asp Val Thr Pro Leu Ser Leu Gly
126 385 390 395 400
129 Ile Glu Thr Met Gly Gly Val Met Thr Thr Leu Ile Ala Lys Asn Thr
130 405 410 415
133 Thr Ile Pro Thr Lys His Ser Gln Val Phe Ser Thr Ala Glu Asp Asn
134 420 425 430
137 Gln Ser Ala Val Thr Ile His Val Leu Gln Gly Glu Arg Lys Arg Ala
138 435 440 445
141 Ala Asp Asn Lys Ser Leu Gly Gln Phe Asn Leu Asp Gly Ile Asn Pro
142 450 455 460
145 Ala Pro Arg Gly Met Pro Gln Ile Glu Val Thr Phe Asp Ile Asp Ala
146 465 470 475 480
149 Asp Gly Ile Leu His Val Ser Ala Lys Asp Lys Asn Ser Gly Lys Glu
150 485 490 495
153 Gln Lys Ile Thr Ile Lys Ala Ser Ser Gly Leu Asn Glu Asp Glu Ile
154 500 505 510
157 Gln Lys Met Val Arg Asp Ala Glu Ala Asn Ala Glu Ala Asp Arg Lys
158 515 520 525
161 Phe Glu Glu Leu Val Gln Thr Arg Asn Gln Gly Asp His Leu Leu His
162 530 535 540
165 Ser Thr Arg Lys Gln Val Glu Glu Ala Gly Asp Lys Leu Pro Ala Asp
166 545 550 555 560
169 Asp Lys Thr Ala Ile Glu Ser Ala Leu Thr Ala Leu Glu Thr Ala Leu
170 565 570 575
173 Lys Gly Glu Asp Lys Ala Ala Ile Glu Ala Lys Met Gln Glu Leu Ala

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174	580	585	590	
177	Gln Val Ser Gln Lys Leu Met Glu Ile Ala Gln Gln Gln His Ala Gln			
178	595	600	605	
181	Gln Gln Thr Ala Gly Ala Asp Ala Ser Ala Asn Asn Ala Lys Asp Asp			
182	610	615	620	
185	Asp Val Val Asp Ala Glu Phe Glu Glu Val Lys Asp Lys Lys			
186	625	630	635	
189	<210> SEQ ID NO: 2			
190	<211> LENGTH: 1917			
191	<212> TYPE: DNA			
192	<213> ORGANISM: Escherichia coli			
194	<400> SEQUENCE: 2			
195	atggtaaaa taattggtat cgacctgggt actaccaact ctttgttagc gattatggat	60		
197	ggcaccactc ctcgcgtgct ggagaacgcc gaaggcgatc gcaccacgcc ttctatcatt	120		
199	gcctataccc agatggtga aactctagtt ggtcagccgg ctaaacgtca ggcagtgacg	180		
201	aacctcgaaa acactctgtt tgcgattaaa cgcctgattt gtcgcccgtt ccaggacgaa	240		
203	gaagtacagc gtgatgtttc catcatgccg ttcaaaaatta ttgctgtga taacggcgac	300		
205	gcatgggtcg aagttaaagg ccagaaaatg gcaccgcccgc agatttctgc tgaagtgctg	360		
207	aaaaaaatga agaaaaccgc tgaagattac ctgggtgaac cggtaactga agctgttatac	420		
209	accgtaccgg catactttaa cgatgcttag cgtcaggcaa ccaaagacgc aggccgtatc	480		
211	gctggctcgg aagtaaaaacg tatcatcaac gaaccgaccg cagctgcgtt ggcttacggt	540		
213	ctggacaaag gcactggcaa ccgtactatc gcggttttagt acctgggtgg tggtaacttac	600		
215	gatatttcta ttatcgaaat cgacgaagtt gacggcgaaa aaaccttcga agttctggca	660		
217	accaacggtg atacccaccc ggggggtgaa gacttcgaca gccgtctgat caactatctg	720		
219	gttgaagaat tcaagaaaaga tcagggcatt gacctgcgc acgatccgct ggcaatgcag	780		
221	cgcctgaaag aagccgcaga aaaagcgaaa atcgaactgt cttccgctca gcagaccgac	840		
223	gttaaacctgc catacatcac tgcagacgc accggccga aacacatgaa catcaaagtg	900		
225	actcgtgcga aactggaaaag cctgggtgaa gatctggtaa accgttccat tgagccgt	960		
227	aaagttgcac tgcaggacgc tggcctgtcc gatatctgata tgcacgcgt tattctcgat	1020		
229	ggtggtcaga ctcgtatgcc aatggttcag aagaaagttt ctgagttctt tggtaaagag	1080		
231	ccgcgtaaag acgttaaccc ggacgaagct gtagcaatcg gtgctgtgt tcaggggtgg	1140		
233	gttctactg gtgacgtaaa agacgtactg ctgctggacg ttaccccgct gtctctgggt	1200		
235	atcgaaacca tggccgggtt gatgacgcg ctgatcgcga aaaacaccac tatccgacc	1260		
237	aagcacagcc aggtgttctc taccgctgaa gacaaccagt ctgcggtaac catccatgt	1320		
239	ctgcagggtg aacgttaacgc tgcggctgat aacaaatctc tgggtcagtt caacctagat	1380		
241	ggtatcaacc cggcacccgc cggcatgccg cagatcgaag ttaccttcga tatcgatgt	1440		
243	gacggtatcc tgcacgttcc cgcgaaagat aaaacagcg gtaaagagca gaagatcacc	1500		
245	atcaaggctt cttctggctt gaaacgaaat gaaatccaga aaatggtacg cgacgcagaa	1560		
247	gctaacgcgc aagctgacccg taagttgaa gagctggatc agactcgcaa ccaggccgac	1620		
249	catctgtgc acagcacccgc taagcagggtt gaaagacgc ggcacaaact gccggctgac	1680		
251	gacaaaactg ctatcgatc tgcgctgact gcaactggaaa ctgctctgaa aggtgaagac	1740		
253	aaagcccta tcgaagcgaa aatgcaggaa ctggcacagg tttcccgaaa actgatggaa	1800		
255	atcgcccagc agcaacatgc ccagcagcag actgcccgtt ctgatgcttc tgcaaacaac	1860		
257	gccaaggatg acgtgttgcg acgtgttgcg tttgaagaag tcaaagacaa aaaataa	1917		
260	<210> SEQ ID NO: 3			
261	<211> LENGTH: 55			
262	<212> TYPE: DNA			
263	<213> ORGANISM: Artificial			
265	<220> FEATURE:			

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266 <223> OTHER INFORMATION: Synthetic DNA
268 <400> SEQUENCE: 3
269 gcggatccat cgagggtaga ggtgacgtaa aagacgtact gctgctggac gttac      55
272 <210> SEQ ID NO: 4
273 <211> LENGTH: 33
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Synthetic DNA
280 <400> SEQUENCE: 4
281 ttatTTTtgcTTTgactt cttcaaattc agc      33
284 <210> SEQ ID NO: 5
285 <211> LENGTH: 30
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Synthetic DNA
292 <400> SEQUENCE: 5
293 gcccggctgac gactaaactg ctatcgagtc      30
296 <210> SEQ ID NO: 6
297 <211> LENGTH: 30
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Synthetic DNA
304 <400> SEQUENCE: 6
305 gactcgatag cagTTtagtc gtcagccggc      30
308 <210> SEQ ID NO: 7
309 <211> LENGTH: 30
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Synthetic DNA
316 <400> SEQUENCE: 7
317 tgctctgaaa ggttaagaca aagccgctat      30
320 <210> SEQ ID NO: 8
321 <211> LENGTH: 30
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Synthetic DNA
328 <400> SEQUENCE: 8
329 atagcggctt tgtcttaacc tttcagagca      30
332 <210> SEQ ID NO: 9
333 <211> LENGTH: 30
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Synthetic DNA

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340 <400> SEQUENCE: 9
341 gcagcaacat gcctaacagc agactgccgg 30
344 <210> SEQ ID NO: 10
345 <211> LENGTH: 30
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial
349 <220> FEATURE:
350 <223> OTHER INFORMATION: Synthetic DNA
352 <400> SEQUENCE: 10
353 ccggcagtct gctttaggc atgttgctgc 30
356 <210> SEQ ID NO: 11
357 <211> LENGTH: 30
358 <212> TYPE: DNA
359 <213> ORGANISM: Artificial
361 <220> FEATURE:
362 <223> OTHER INFORMATION: Synthetic DNA
364 <400> SEQUENCE: 11
365 ccttcgatat cgttgctgtc ggtatcctgc 30
368 <210> SEQ ID NO: 12
369 <211> LENGTH: 30
370 <212> TYPE: DNA
371 <213> ORGANISM: Artificial
373 <220> FEATURE:
374 <223> OTHER INFORMATION: Synthetic DNA
376 <400> SEQUENCE: 12
377 gcaggatacc gacagcaacg atatcgaagg 30
380 <210> SEQ ID NO: 13
381 <211> LENGTH: 27
382 <212> TYPE: DNA
383 <213> ORGANISM: Artificial
385 <220> FEATURE:
386 <223> OTHER INFORMATION: Synthetic DNA
388 <400> SEQUENCE: 13
389 tctggatcca acgaagatga aatccag 27
392 <210> SEQ ID NO: 14
393 <211> LENGTH: 30
394 <212> TYPE: DNA
395 <213> ORGANISM: Artificial
397 <220> FEATURE:
398 <223> OTHER INFORMATION: Synthetic DNA
400 <400> SEQUENCE: 14
401 gcgatccgc tgaccgttaag tttgaagagc 30
404 <210> SEQ ID NO: 15
405 <211> LENGTH: 29
406 <212> TYPE: DNA
407 <213> ORGANISM: Artificial
409 <220> FEATURE:
410 <223> OTHER INFORMATION: Synthetic DNA
412 <400> SEQUENCE: 15

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/10/2006
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17

VERIFICATION SUMMARY
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Input Set : A:\248832.ST25.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date